

OIEP

RAW SEQUENCE LISTING

DATE: 01/10/2002

PATENT APPLICATION: US/10/022,710

TIME: 14:42:04

Input Set : A:\LEX-0290-USA SEQLIST.txt

Output Set: N:\CRF3\01102002\J022710.raw

ENTERED

4 <110> APPLICANT: Friddle, Carl Johan
 5 Aylor, Erin
 6 Walke, D. Wade
 8 <120> TITLE OF INVENTION: Novel Human Thrombospondin Repeat
 9 Proteins and Polynucleotides Encoding the Same
 12 <130> FILE REFERENCE: LEX-0290-USA
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/022,710
 C--> 14 <141> CURRENT FILING DATE: 2001-12-13
 14 <150> PRIOR APPLICATION NUMBER: US 60/259,033
 15 <151> PRIOR FILING DATE: 2000-12-28
 17 <160> NUMBER OF SEQ ID NOS: 7
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 4398
 23 <212> TYPE: DNA
 24 <213> ORGANISM: homo sapiens
 26 <400> SEQUENCE: 1

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28 ttgccccttc agcctcctac agaacaggct tgccctcattc cttgtccccg ggattgtgta 120
29 gtatctgagt tcttaccatg gtccaactgt agcaagggat gtgggaagaa attgcagcat 180
30 agaactcgcg cggatcatagc tccccctctc tttggtggtt tgcaatgtcc aaatctgact 240
31 gagtcaagag cctgtgatgc tcccatttcc tgtcctcttg gggaagagga atatacattt 300
32 agccttaagg ttggaccatg gagtaaatgc agactgcctc atcttaaaga aattaatcca 360
33 agcggaaagaa ctgttctgga ttttaactct gattcaaatg agcgagtcac ctttaaacad 420
34 caaagttaca aagcacatca tcattcgaag tcttgggcaa tagagatagg ttatcaaac 480
35 cggcagggtt cgtgtacaag aagtgatgga caaaatgcta tgtaagcct ttgccttcaa 540
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37 tggtcctcct ggagcccctg ctccaagaca tgccgttcag ggagtctctt gccaggattt 660
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42 tgtgcccaga gcgtaccagc agctgccgca ctgagggcca aggaagtctc tagacctgtg 960
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56 actcgacctg aaactgtgcg cccctgtttt ctcccatgca aaaaagactg tattgtgact 1800

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57 gcttttcagtg agtggacacc ctgcccgaagg atgtgccaag caggaaatgc cacagtaaaa 1860
58 cagtctcgat acagaatcat catccaagaa gcagccaatg gaggccagga atgcccgat 1920
59 accttatatg aggagagaga gtgtgaagat gtttccttgt gtcctgtata tcggtggaag 1980
60 ccacagaaat ggagcccttg catcttagtg ccagagctctg tctggcaggg aataacgggc 2040
61 agcagtgaag cctgtggaaa ggggttacaa acaagagctg tctcatgcat ctctgatgac 2100
62 aaccggtcag cagaaatgat ggaatgcctc aagcagacaa acggcatgcc tctccttgtg 2160
63 caagaatgca cagtcccctg tcgagaagac tgcaccttca ctgcttggtc caagtttacg 2220
64 ccctgctcca cgaactgtga agccacaaaa agtaggcggc gacagctcac agggaaaagc 2280
65 agaaaagaagg agaaatgcca ggattctgac ctttaccctc tagtggagac agaactatgt 2340
66 ccttgtgatg aatttatatc ccaaccttat ggaaactggg cagattgcat tcttcagaa 2400
67 ggcagaaggg agcctcaccg aggactgcgg gtacaagcag acagcaaaga atgtggagaa 2460
68 ggcctgcgct ttcgagcagt agcctgttct gataaaaatg gaagacctgt tgaccctcc 2520
69 ttctgcagca gctctgggta cattcaagaa aaatgtgtca ttccctgccc atttgattgc 2580
70 aagttaagcg attggtctag ttgggggtct tgcagttcat cttgtggaat tggagtgaga 2640
71 attcgatcca aatggctaaa agaaaaacct tacaatggag gacgacctg tcccaaactg 2700
72 gatctcaaga atcaggtaca tgaggcagtc ccatgttaca gtgagtgcaa tcagtattcc 2760
73 tgggtttagt aacactggtc ttcatgcaaa atcaacaatg agctgaggtc cctgcgctgt 2820
74 ggaggaggaa cacaatctag gaaaatcaga tgtgtgaata ctgcggatgg tgaagggtga 2880
75 gcagtggata gcaacctgtg caaccaggat gaaattcccc cagaaacca gtccgttct 2940
76 cttatgtgtc ccaatgagtg tgtcatgtct gagtggggac tttggagcaa atgccacag 3000
77 tcatgcgac cccacacaaat gcagagaaga actcgccacc tgctaagacc atcactgaac 3060
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84 gaaggacggc catgccccac agagcttacc caggagaaaa cctgcccagt gacccctgc 3480
85 tacagctggg tccttggcaa ctggtctgca tgtaaaattg aggggtggaga ctgtggggaa 3540
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90 aggactttta taattcagtc ttttgagaac caagacagct gcccccaaca ggttctagaa 3840
91 acacgccctt gtacaggagg caaatgttat cactacacat ggaaagcaag tctttggaac 3900
92 aataacgaac gaactgtatg gtgccagcgt tcagatggcg ttaatgtcac aggaggtgc 3960
93 tcccctcagg cccgtcctgc tgcattcgg cagtgcattc cagcctgcag aaaaccttcc 4020
94 tcctactgta cacagggtgg agtctgtggt tgtgagaagg gctatacaga gataatgaaa 4080
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100 ggagacttag acatgtaa 4398
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 1465
104 <212> TYPE: PRT
105 <213> ORGANISM: homo sapiens
107 <400> SEQUENCE: 2

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108 Met Val Arg Cys Ile Gln Lys Leu Asn Arg Thr Val Val Ala Asn Glu
109 1 5 10 15
110 Ile Cys Glu His Phe Ala Leu Gln Pro Thr Glu Gln Ala Cys Leu
111 20 25 30
112 Ile Pro Cys Pro Arg Asp Cys Val Val Ser Glu Phe Leu Pro Trp Ser
113 35 40 45
114 Asn Cys Ser Lys Gly Cys Gly Lys Lys Leu Gln His Arg Thr Arg Ala
115 50 55 60
116 Val Ile Ala Pro Pro Leu Phe Gly Gly Leu Gln Cys Pro Asn Leu Thr
117 65 70 75 80
118 Glu Ser Arg Ala Cys Asp Ala Pro Ile Ser Cys Pro Leu Gly Glu Glu
119 85 90 95
120 Glu Tyr Thr Phe Ser Leu Lys Val Gly Pro Trp Ser Lys Cys Arg Leu
121 100 105 110
122 Pro His Leu Lys Glu Ile Asn Pro Ser Gly Arg Thr Val Leu Asp Phe
123 115 120 125
124 Asn Ser Asp Ser Asn Glu Arg Val Thr Phe Lys His Gln Ser Tyr Lys
125 130 135 140
126 Ala His His His Ser Lys Ser Trp Ala Ile Glu Ile Gly Tyr Gln Thr
127 145 150 155 160
128 Arg Gln Val Ser Cys Thr Arg Ser Asp Gly Gln Asn Ala Met Leu Ser
129 165 170 175
130 Leu Cys Leu Gln Asp Ser Phe Pro Leu Thr Val Gln Ser Cys Ile Met
131 180 185 190
132 Pro Lys Asp Cys Glu Thr Ser Gln Trp Ser Ser Trp Ser Pro Cys Ser
133 195 200 205
134 Lys Thr Cys Arg Ser Gly Ser Leu Leu Pro Gly Phe Arg Ser Arg Ser
135 210 215 220
136 Arg Asn Val Lys His Met Ala Ile Gly Gly Gly Lys Glu Cys Pro Glu
137 225 230 235 240
138 Leu Leu Glu Lys Glu Ala Cys Ile Val Glu Gly Glu Leu Leu Gln Gln
139 245 250 255
140 Cys Pro Arg Tyr Ser Trp Arg Thr Ser Glu Trp Lys Glu Cys Gln Val
141 260 265 270
142 Ser Leu Leu Glu Gln Gln Asp Pro His Trp His Val Thr Gly Pro
143 275 280 285
144 Val Cys Gly Gly Gly Ile Gln Thr Arg Glu Val Tyr Cys Ala Gln Ser
145 290 295 300
146 Val Pro Ala Ala Ala Ala Leu Arg Ala Lys Glu Val Ser Arg Pro Val
147 305 310 315 320
148 Glu Lys Ala Leu Cys Val Gly Pro Ala Pro Leu Pro Ser Gln Leu Cys
149 325 330 335
150 Asn Ile Pro Cys Ser Thr Asp Cys Ile Val Ser Ser Trp Ser Ala Trp
151 340 345 350
152 Gly Leu Cys Ile His Glu Asn Cys His Glu Pro Gln Gly Lys Lys Gly
153 355 360 365
154 Phe Arg Thr Arg Gln Arg His Val Leu Met Glu Ser Thr Gly Pro Ala
155 370 375 380
156 Gly His Cys Pro His Leu Val Glu Ser Val Pro Cys Glu Asp Pro Met

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157 385          390          395          400
158 Cys Tyr Arg Trp Leu Ala Ser Glu Gly Ile Cys Phe Pro Asp His Gly
159          405          410          415
160 Lys Cys Gly Leu Gly His Arg Ile Leu Lys Ala Val Cys Gln Asn Asp
161          420          425          430
162 Arg Gly Glu Asp Val Ser Gly Ser Leu Cys Pro Val Pro Pro Pro
163          435          440          445
164 Glu Arg Lys Ser Cys Glu Ile Pro Cys Arg Met Asp Cys Val Leu Ser
165          450          455          460
166 Glu Trp Thr Glu Trp Ser Ser Cys Ser Gln Ser Cys Ser Asn Lys Asn
167 465          470          475          480
168 Ser Asp Gly Lys Gln Thr Arg Ser Arg Thr Ile Leu Ala Leu Ala Gly
169          485          490          495
170 Glu Gly Gly Lys Pro Cys Pro Pro Ser Gln Ala Leu Gln Glu His Arg
171          500          505          510
172 Leu Cys Asn Asp His Ser Cys Met Gln Leu His Trp Glu Thr Ser Pro
173          515          520          525
174 Trp Gly Pro Cys Ser Glu Asp Thr Leu Val Thr Ala Leu Asn Ala Thr
175          530          535          540
176 Ile Gly Trp Asn Gly Glu Ala Thr Cys Gly Val Gly Ile Gln Thr Arg
177 545          550          555          560
178 Arg Val Phe Cys Val Lys Ser His Val Gly Gln Val Met Thr Lys Arg
179          565          570          575
180 Cys Pro Asp Ser Thr Arg Pro Glu Thr Val Arg Pro Cys Phe Leu Pro
181          580          585          590
182 Cys Lys Lys Asp Cys Ile Val Thr Ala Phe Ser Glu Trp Thr Pro Cys
183          595          600          605
184 Pro Arg Met Cys Gln Ala Gly Asn Ala Thr Val Lys Gln Ser Arg Tyr
185          610          615          620
186 Arg Ile Ile Ile Gln Glu Ala Ala Asn Gly Gly Gln Glu Cys Pro Asp
187 625          630          635          640
188 Thr Leu Tyr Glu Glu Arg Glu Cys Glu Asp Val Ser Leu Cys Pro Val
189          645          650          655
190 Tyr Arg Trp Lys Pro Gln Lys Trp Ser Pro Cys Ile Leu Val Pro Glu
191          660          665          670
192 Ser Val Trp Gln Gly Ile Thr Gly Ser Ser Glu Ala Cys Gly Lys Gly
193          675          680          685
194 Leu Gln Thr Arg Ala Val Ser Cys Ile Ser Asp Asp Asn Arg Ser Ala
195          690          695          700
196 Glu Met Met Glu Cys Leu Lys Gln Thr Asn Gly Met Pro Leu Leu Val
197 705          710          715          720
198 Gln Glu Cys Thr Val Pro Cys Arg Glu Asp Cys Thr Phe Thr Ala Trp
199          725          730          735
200 Ser Lys Phe Thr Pro Cys Ser Thr Asn Cys Glu Ala Thr Lys Ser Arg
201          740          745          750
202 Arg Arg Gln Leu Thr Gly Lys Ser Arg Lys Lys Glu Lys Cys Gln Asp
203          755          760          765
204 Ser Asp Leu Tyr Pro Leu Val Glu Thr Glu Leu Cys Pro Cys Asp Glu
205          770          775          780

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206 Phe Ile Ser Gln Pro Tyr Gly Asn Trp Ser Asp Cys Ile Leu Pro Glu
207 785 790 795 800
208 Gly Arg Arg Glu Pro His Arg Gly Leu Arg Val Gln Ala Asp Ser Lys
209 805 810 815
210 Glu Cys Gly Glu Gly Leu Arg Phe Arg Ala Val Ala Cys Ser Asp Lys
211 820 825 830
212 Asn Gly Arg Pro Val Asp Pro Ser Phe Cys Ser Ser Ser Gly Tyr Ile
213 835 840 845
214 Gln Glu Lys Cys Val Ile Pro Cys Pro Phe Asp Cys Lys Leu Ser Asp
215 850 855 860
216 Trp Ser Ser Trp Gly Ser Cys Ser Ser Ser Cys Gly Ile Gly Val Arg
217 865 870 875 880
218 Ile Arg Ser Lys Trp Leu Lys Glu Lys Pro Tyr Asn Gly Gly Arg Pro
219 885 890 895
220 Cys Pro Lys Leu Asp Leu Lys Asn Gln Val His Glu Ala Val Pro Cys
221 900 905 910
222 Tyr Ser Glu Cys Asn Gln Tyr Ser Trp Val Val Glu His Trp Ser Ser
223 915 920 925
224 Cys Lys Ile Asn Asn Glu Leu Arg Ser Leu Arg Cys Gly Gly Gly Thr
225 930 935 940
226 Gln Ser Arg Lys Ile Arg Cys Val Asn Thr Ala Asp Gly Glu Gly Gly
227 945 950 955 960
228 Ala Val Asp Ser Asn Leu Cys Asn Gln Asp Glu Ile Pro Pro Glu Thr
229 965 970 975
230 Gln Ser Cys Ser Leu Met Cys Pro Asn Glu Cys Val Met Ser Glu Trp
231 980 985 990
232 Gly Leu Trp Ser Lys Cys Pro Gln Ser Cys Asp Pro His Thr Met Gln
233 995 1000 1005
234 Arg Arg Thr Arg His Leu Leu Arg Pro Ser Leu Asn Ser Arg Thr Cys
235 1010 1015 1020
236 Ala Glu Asp Ser Gln Val Gln Pro Cys Leu Leu Asn Glu Asn Cys Phe
237 1025 1030 1035 1040
238 Gln Phe Gln Tyr Asn Leu Thr Glu Trp Ser Thr Cys Gln Leu Ser Glu
239 1045 1050 1055
240 Asn Ala Pro Cys Gly Gln Gly Val Arg Thr Arg Leu Leu Ser Cys Val
241 1060 1065 1070
242 Cys Ser Asp Gly Lys Pro Val Ser Met Asp Gln Cys Glu Gln His Asn
243 1075 1080 1085
244 Leu Glu Lys Pro Gln Arg Met Ser Ile Pro Cys Leu Val Glu Cys Val
245 1090 1095 1100
246 Val Asn Cys Gln Leu Ser Gly Trp Thr Ala Trp Thr Glu Cys Ser Gln
247 1105 1110 1115 1120
248 Thr Cys Gly His Gly Gly Arg Met Ser Arg Thr Arg Phe Ile Ile Met
249 1125 1130 1135
250 Pro Thr Gln Gly Glu Gly Arg Pro Cys Pro Thr Glu Leu Thr Gln Glu
251 1140 1145 1150
252 Lys Thr Cys Pro Val Thr Pro Cys Tyr Ser Trp Val Leu Gly Asn Trp
253 1155 1160 1165
254 Ser Ala Cys Lys Leu Glu Gly Gly Asp Cys Gly Glu Gly Val Gln Ile

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→ Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/022,710

DATE: 01/10/2002

TIME: 14:42:06

Input Set : A:\LEX-0290-USA SEQLIST.txt

Output Set: N:\CRF3\01102002\J022710.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7